

1/4

10 30 50
CACGAGGACAACAGTACCTGACGCCTCTTTCAGCCCGGGATCGCCCCAGCAGGGATGGGC
M G

70 90 110
GACAAGATCTGGCTGCCCTTCCCCGTGCTCCTTCTGGCCGCTCTGCCTCCGGTGCTGCTG
D K I W L P F P V L L L A A L P P V L L

130 150 170
CCTGGGGCGGCCGGCTTCACACCTTCCCTCGATAGCGACTTCACCTTTACCTTCCCGCC
P G A A G F T P S L D S D F T F T L P A

190 210 230
GGCCAGAAGGAGTGCTTCTACCAGCCCATGCCCTGAAGGCCTCGCTGGAGATCGAGTAC
G Q K E C F Y Q P M P L K A S L E I E Y

250 270 290
CAAGTTTTAGATGGAGCAGGATTAGATATTGATTTCCATCTTGCCTCTCCAGAAGGCAAA
Q V L D G A G L D I D F H L A S P E G K

310 330 350
ACCTTAGTTTTTTGAACAAAGAAAATCAGATGGAGTTCACACTGTAGAGACTGAAGTTGGT
T L V F E Q R K S D G V H T V E T E V G

370 390 410
GATTACATGTTCTGCTTTGACAATACATTTCAGCACCATTTCTGAGAAGGTGATTTTCTTT
D Y M F C F D N T F S T I S E K V I F F

430 450 470
GAATTAATCCTGGATAATATGGGAGAACAGGCACAAGAACAAGAAGATTGGAAGAAATAT
E L I L D N M G E Q A Q E Q E D W K K Y

490 510 530
ATTACTGGCACAGATATATTGGATATGAAACTGGAAGACATCCTGGAATCCATCAACAGC
I T G T D I L D M K L E D I L E S I N S

550 570 590
ATCAAGTCCAGACTAAGCAAAAGTGGGCACATACAAACTCTGCTTAGAGCATTTGAAGCT
I K S R L S K S G H I Q T L L R A F E A

FIG.1A

610	630	650
CGTGATCGAAACATACAAGAAAGCAACTTTGATAGAGTCAATTTCTGGTCTATGGTTAAT		
R D R N I Q E S N F D R	<u>V N F W S M V N</u>	
670	690	710
TTAGTGGTCATGGTGGTGGTGTGAGCCATTCAAGTTTATATGCTGAAGAGTCTGTTTGAA		
<u>L V V M V V V S A I Q V Y M L</u>	K S L F E	
730	750	770
GATAAGAGGAAAAAGTAGAACTTAAAACTCCAACTAGAGTACGTAACATTGAAAAATGAG		
D K R K S R T *		
790	810	830
GCATAAAAATGCCATAAACTGTTACAGTCCAGACCATTAATGGTCTTCTCCAAAATATTT		
850	870	890
TGAGATATAAAAAGTAGGAAACAGGTATAATTTTAATGTGAAAATTAAGTCTTCACTTTCT		
910	930	950
GTGCAAGTAATCCTGCTGATCCAGTTGTACTTAAGTGTGTAACAGGAATATTTTGCAGAA		
970	990	1010
TATAGGTTTAACTGAATGAAGCCATATTAATAACTGCATTTTCCTAACTTTGAAAAATTT		
1030	1050	1070
TGCAAATGTCTTAGGTGATTTAAATAAATGAGTATTGGGCCTAATTGCAACACCAGTCTG		
1090	1110	1130
TTTTTAAACAGGTTCTATTACCCAGAACTTTTTTGTAATGCGGCAGTTACAAATTAAGT		
1150	1170	1190
TGGAAGTTTTTCAGTTTTAAGTTATAAATCACCTGAGAATTACCTAATGATGGATTGAATA		
1210	1230	
AATCTTTAGACTACAAAAA		

FIG.1B

1	.MGDKIWLPPFPVLLLAALPPVLLPGAAGFTPSLDSDFTFLLPAGQKECFY	49
	: . ::: : : : . :: . :	
1	MMAAGAALALALWLL. .MPPVEV.GGAGPPPIQDGEFTFLLPAGRKQCFY	47
50	QPMPLKASLEIEYQVLDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVE.	98
	. . . : : : : . : .	
48	QSAPANASLETEYQVIGGAGLDVDFTLSPQGVLLVSESARKADGVHTVEP	97
99	TEVGDMFCFDNTFSTISEKVIFFELILDNMGEQAQEQEDWKYITGTDI	148
	. . : . : : : : . : : : : : : . : : : : :	
98	TEAGDYKLCFDNSFSTISEKLVFFELIFDSLQDD. EEVEGWAEAVEPEEM	146
149	LDMKLEDILESINSIKSRLSKSGHIQTLLRAFEARDRNIQESNFDRVNF	198
	: : : : : . . : : : : : : :	
147	LDVKMEDIKESIETMRTRLERSIQMLTLLRAFEARDRNLQEGNLERVNF	196
199	SMVNLVVMVVSAIQVYMLKSLFEDKRKSRT. 229	
	: . : : . : : . : : . .	
197	SAVNVAVLLLVAVLQVCTLKRFFQDKRPVPT. 227	

FIG.2

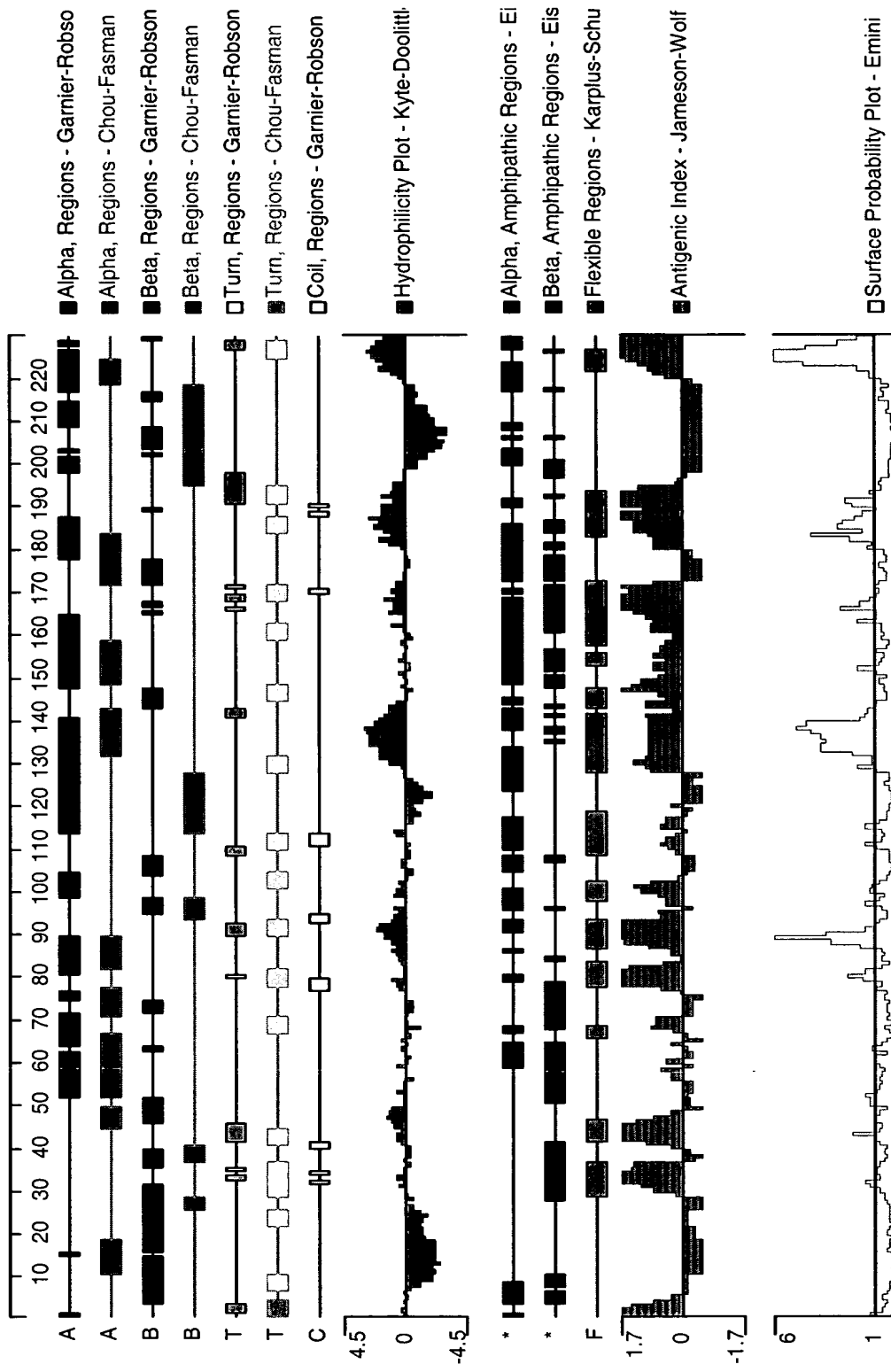


FIG.3